Supplemental Material

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##   
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':  
##   
## filter, lag

## The following objects are masked from 'package:base':  
##   
## intersect, setdiff, setequal, union

## here() starts at /Users/miacarmichael/Desktop/epid8060fall2019/MiaCarmichael-Project

## Loading required package: carData

##   
## Attaching package: 'car'

## The following object is masked from 'package:dplyr':  
##   
## recode

## Loading required package: lattice

##   
## Attaching package: 'vip'

## The following object is masked from 'package:utils':  
##   
## vi

## Loading required package: ParamHelpers

##   
## Attaching package: 'mlr'

## The following object is masked from 'package:caret':  
##   
## train

##   
## Attaching package: 'ggstance'

## The following objects are masked from 'package:ggplot2':  
##   
## geom\_errorbarh, GeomErrorbarh

##   
## Attaching package: 'huxtable'

## The following object is masked from 'package:ggplot2':  
##   
## theme\_grey

## The following object is masked from 'package:pander':  
##   
## wrap

## The following object is masked from 'package:dplyr':  
##   
## add\_rownames

## ── Attaching packages ───────────────────────────────────────────────────────────────── tidyverse 1.2.1 ──

## ✔ tibble 2.1.3 ✔ purrr 0.3.2  
## ✔ tidyr 1.0.0 ✔ stringr 1.4.0  
## ✔ tibble 2.1.3 ✔ forcats 0.4.0

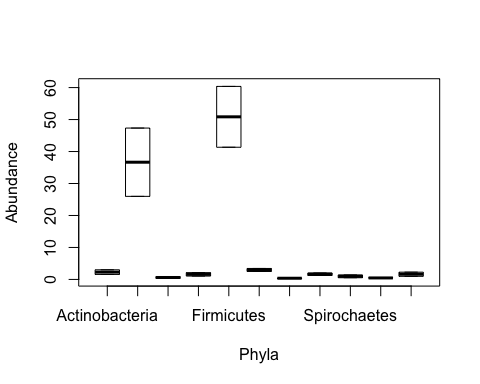
## ── Conflicts ──────────────────────────────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ huxtable::add\_rownames() masks dplyr::add\_rownames()  
## ✖ purrr::every() masks huxtable::every()  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ ggstance::geom\_errorbarh() masks ggplot2::geom\_errorbarh()  
## ✖ dplyr::lag() masks stats::lag()  
## ✖ purrr::lift() masks caret::lift()  
## ✖ car::recode() masks dplyr::recode()  
## ✖ purrr::some() masks car::some()  
## ✖ huxtable::theme\_grey() masks ggplot2::theme\_grey()

## Bivariate Analysis

Bacterial abundance verses time period. ANOVA allows us to see that there is variance between the bacterial abundance at beginning and end of the feedlot period in High-RFI steers (Table 5, Table 6). This indicates that the microbiome did experieience changes over the course of the feedlot period.

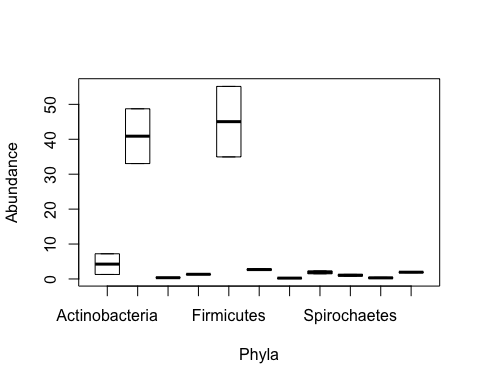
Looking at the correlation, we can see that there is a high positive correlation between the change from the beginning of the feedlot period to the end of the feeddlot period for phyla, and therefore the correlation between them will be closer to 1.

# Looking at ANOVA



## Df Sum Sq Mean Sq F value Pr(>F)   
## Phyla 10 6089 608.9 16.22 3.43e-05 \*\*\*  
## Residuals 11 413 37.5   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Df Sum Sq Mean Sq F value Pr(>F)   
## Phyla 10 6089 608.9 16.22 3.43e-05 \*\*\*  
## Residuals 11 413 37.5   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



## Df Sum Sq Mean Sq F value Pr(>F)   
## Phyla 10 5655 565.5 18.02 2.03e-05 \*\*\*  
## Residuals 11 345 31.4   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## Df Sum Sq Mean Sq F value Pr(>F)   
## Phyla 10 5655 565.5 18.02 2.03e-05 \*\*\*  
## Residuals 11 345 31.4   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# Looking at a correlation between data points at the beginning and end of feedlot period

##   
## Attaching package: 'flextable'

## The following object is masked from 'package:purrr':  
##   
## compose

## The following objects are masked from 'package:huxtable':  
##   
## align, as\_flextable, bold, font, height, italic, set\_caption,  
## valign, width

|  |
| --- |
| **x** |
| 0.874 |

|  |
| --- |
| **x** |
| 0.888 |

# Looking at Linear Model

##   
## Call:  
## lm(formula = Beginning ~ End, data = phylatest)  
##   
## Coefficients:  
## (Intercept) End   
## 1.5911 0.8251

##   
## Call:  
## lm(formula = Beginning ~ End, data = phylatest)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -10.060 -2.150 -1.931 -1.046 24.314   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.5911 3.0335 0.525 0.612600   
## End 0.8251 0.1526 5.408 0.000429 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 8.948 on 9 degrees of freedom  
## Multiple R-squared: 0.7647, Adjusted R-squared: 0.7385   
## F-statistic: 29.25 on 1 and 9 DF, p-value: 0.0004286

|  |  |  |  |
| --- | --- | --- | --- |
| **Sum Sq** | **Df** | **F value** | **Pr(>F)** |
| 22 | 1 | 0.275 | 0.613 |
| 2.34e+03 | 1 | 29.2 | 0.000429 |
| 721 | 9 |  |  |

##   
## Call:  
## lm(formula = Beginning ~ End, data = phylatest)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -10.060 -2.150 -1.931 -1.046 24.314   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.5911 3.0335 0.525 0.612600   
## End 0.8251 0.1526 5.408 0.000429 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 8.948 on 9 degrees of freedom  
## Multiple R-squared: 0.7647, Adjusted R-squared: 0.7385   
## F-statistic: 29.25 on 1 and 9 DF, p-value: 0.0004286

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | 1.59 | 3.03 | 0.525 | 0.613 |
| End | 0.825 | 0.153 | 5.41 | 0.000429 |

##   
## Call:  
## lm(formula = Beginning ~ End, data = phylatest2)  
##   
## Coefficients:  
## (Intercept) End   
## 1.653 0.818

##   
## Call:  
## lm(formula = Beginning ~ End, data = phylatest2)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -11.807 -1.766 -1.533 -1.258 20.050   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.6529 2.7449 0.602 0.561918   
## End 0.8180 0.1412 5.792 0.000262 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 8.046 on 9 degrees of freedom  
## Multiple R-squared: 0.7885, Adjusted R-squared: 0.7649   
## F-statistic: 33.54 on 1 and 9 DF, p-value: 0.0002622

|  |  |  |  |
| --- | --- | --- | --- |
| **Sum Sq** | **Df** | **F value** | **Pr(>F)** |
| 23.5 | 1 | 0.363 | 0.562 |
| 2.17e+03 | 1 | 33.5 | 0.000262 |
| 583 | 9 |  |  |

##   
## Call:  
## lm(formula = Beginning ~ End, data = phylatest2)  
##   
## Residuals:  
## Min 1Q Median 3Q Max   
## -11.807 -1.766 -1.533 -1.258 20.050   
##   
## Coefficients:  
## Estimate Std. Error t value Pr(>|t|)   
## (Intercept) 1.6529 2.7449 0.602 0.561918   
## End 0.8180 0.1412 5.792 0.000262 \*\*\*  
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
##   
## Residual standard error: 8.046 on 9 degrees of freedom  
## Multiple R-squared: 0.7885, Adjusted R-squared: 0.7649   
## F-statistic: 33.54 on 1 and 9 DF, p-value: 0.0002622

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | 1.65 | 2.74 | 0.602 | 0.562 |
| End | 0.818 | 0.141 | 5.79 | 0.000262 |

## Full Analysis

# K- means Cluster Analysis

Clustering helps find subgroups of observations within a data set. By clustering observations, the desired outcome is to have observations in the same group to be similar and observations in different groups to be dissimilar. Therefor, this method seeks to find relationships between the observations without being trained by a response variable. Finally clustering allows the idenification of which observations are alike and further categorize them.

## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa

# Phyla

|  |  |  |  |
| --- | --- | --- | --- |
| **Phyla** | **Beginning** | **End** | **P** |
| Firmicutes | 41.3 | 60.4 | 0.02 |
| Bacteroidetes | 47.3 | 26 | 0.12 |
| Actinobacteria | 3.01 | 1.56 | 0.34 |
| TM7 | 0.97 | 2.27 | 0.85 |
| Proteobacteria | 1.24 | 2.01 | 0.43 |
| Euryarchaeota | 1.05 | 2.12 | 0.83 |
| Spirochaetes | 1.4 | 0.53 | 0.42 |
| Cyanobacteria | 0.32 | 0.89 | 0.74 |
| Tenericutes | 0.49 | 0.44 | 0.2 |
| Planctomycetes | 0.35 | 0.39 | 0.55 |
| Other Phyla | 2.49 | 3.43 | 0.55 |
| Firmicutes | 35 | 55.1 | 0.02 |
| Bacteroidetes | 48.7 | 33 | 0.12 |
| Actinobacteria | 7.21 | 1.29 | 0.34 |
| TM7 | 1.81 | 2.06 | 0.85 |
| Proteobacteria | 1.48 | 2.31 | 0.43 |
| Euryarchaeota | 1.28 | 1.39 | 0.83 |
| Spirochaetes | 1.31 | 0.81 | 0.42 |
| Cyanobacteria | 0.39 | 0.33 | 0.74 |
| Tenericutes | 0.16 | 0.46 | 0.2 |
| Planctomycetes | 0.21 | 0.27 | 0.55 |
| Other Phyla | 2.46 | 2.91 | 0.55 |

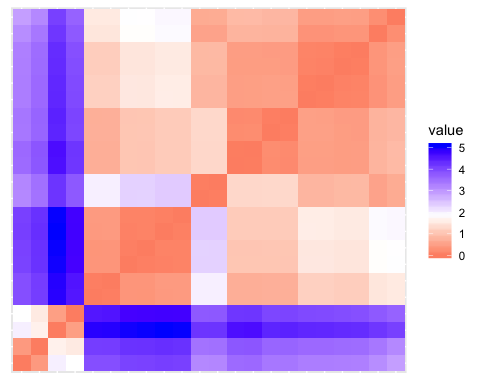
## Phyla Beginning End P   
## "character" "numeric" "numeric" "numeric"

## Beginning End P  
## H-Firmicutes 1.9377655 2.8740021 -1.6138282  
## H-Bacteroidetes 2.2982850 0.9465707 -1.2462897  
## H-Actinobacteria -0.3653538 -0.4220794 -0.4377050  
## H-Proteobacteria -0.4879305 -0.3822866 1.4367415  
## H-Euryarchaeota -0.4717071 -0.3968586 -0.1069203  
## H-TM7 -0.4831236 -0.3906935 1.3632338

Clutering Distance Measures get\_dist: for computing a distance matrix between the rows of a data matrix. fviz\_dist: for visualizing a distance matrix

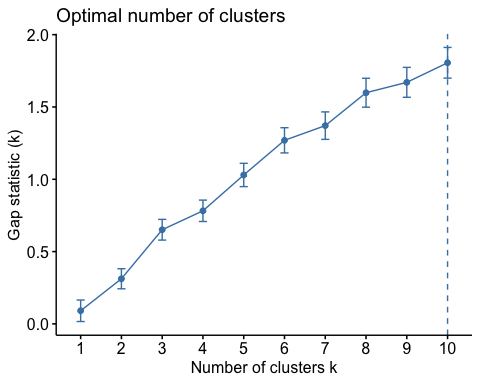
Assessing Clusterability

## [1] 0.9609811

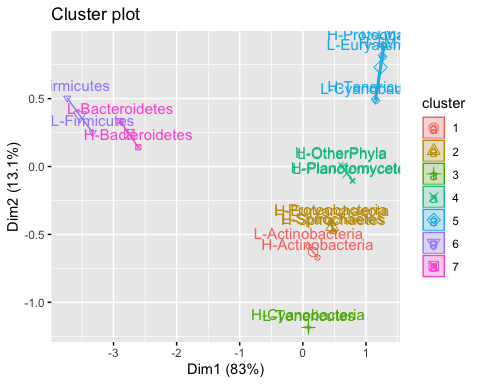


## Saving 5 x 4 in image

The value of the Hopkins statistic is significantly < 0.5 (0.94368), indicating that the data is highly clusterable. Additionally, It can be seen that the ordered dissimilarity image contains patterns (i.e., clusters).

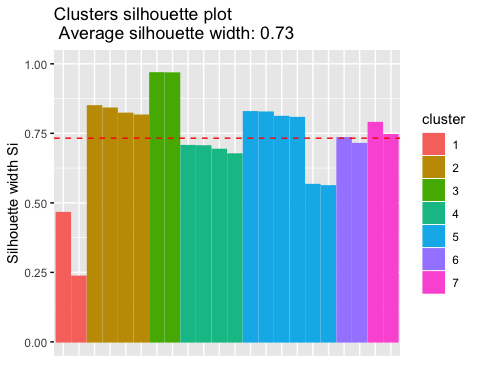
Estimate the number of clusters in the data, method 1 

## H-Firmicutes H-Bacteroidetes H-Actinobacteria H-Proteobacteria   
## 6 7 1 5   
## H-Euryarchaeota H-TM7 H-Spirochaetes H-Tenericutes   
## 2 5 2 5   
## H-Cyanobacteria H-Planctomycetes H-OtherPhyla L-Firmicutes   
## 3 4 4 6   
## L-Bacteroidetes L-Actinobacteria L-TM7 L-Proteobacteria   
## 7 1 5 2   
## L-Euryarchaeota L-Spirochaetes L-Cyanobacteria L-Tenericutes   
## 5 2 5 3   
## L-Planctomycetes L-OtherPhyla   
## 4 4



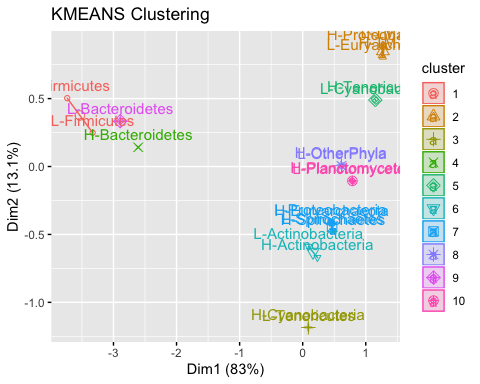
## [1] 6 7 1 5 2 5

## cluster size ave.sil.width  
## 1 1 2 0.35  
## 2 2 4 0.83  
## 3 3 2 0.97  
## 4 4 4 0.69  
## 5 5 6 0.73  
## 6 6 2 0.72  
## 7 7 2 0.77



## cluster neighbor sil\_width

K-means clustering using eclust(), method 2



## cluster size ave.sil.width  
## 1 1 2 0.70  
## 2 2 4 0.81  
## 3 3 2 0.97  
## 4 4 1 0.00  
## 5 5 2 0.92  
## 6 6 2 0.35  
## 7 7 4 0.83  
## 8 8 2 0.86  
## 9 9 1 0.00  
## 10 10 2 0.95

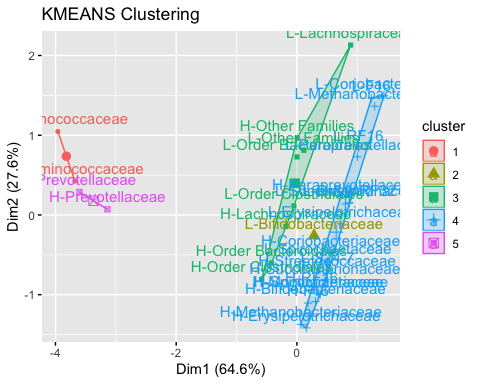
## cluster size ave.sil.width  
## 1 1 1 0.00  
## 2 2 1 0.00  
## 3 3 2 0.35  
## 4 4 4 0.81  
## 5 5 4 0.83  
## 6 6 2 0.92  
## 7 7 2 0.97  
## 8 8 4 0.69  
## 9 9 1 0.00  
## 10 10 1 0.00

Choose a method and do for all (phyla, family, and genus) # Family

## Family Beginning End P   
## "character" "numeric" "numeric" "numeric"

|  |  |  |
| --- | --- | --- |
| **Beginning** | **End** | **P** |
| 26 | 40.3 | 0.17 |
| 36.9 | 14.3 | 0.05 |
| 5.93 | 8.4 | 0.08 |
| 5.94 | 7.49 | 0.15 |
| 5.19 | 7.7 | 0.29 |
| 1.94 | 1.36 | 0.14 |

## [1] 0.8934922



## cluster size ave.sil.width  
## 1 1 2 0.78  
## 2 2 1 0.00  
## 3 3 8 0.77  
## 4 4 22 0.82  
## 5 5 2 0.78

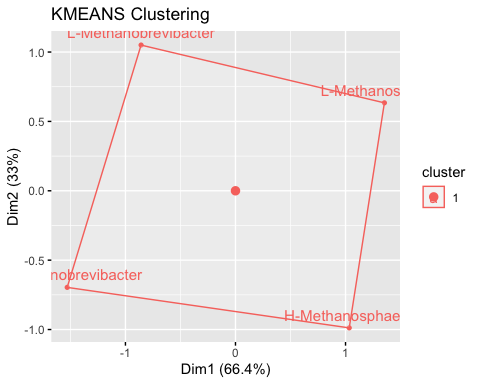
## cluster size ave.sil.width  
## 1 1 2 0.78  
## 2 2 2 0.78  
## 3 3 8 0.80  
## 4 4 23 0.84

# Genus

## Genus Beginning End P   
## "character" "numeric" "numeric" "numeric"

## Beginning End P  
## H-Methanobrevibacter 0.7945875 1.1402255 -0.9504322  
## H-Methanosphaera -0.8715960 -0.8344947 -0.7766388  
## L-Methanobrevibacter 0.9346030 0.5387879 0.8309493  
## L-Methanosphaera -0.8575945 -0.8445187 0.8961217

## [1] 0.3936389

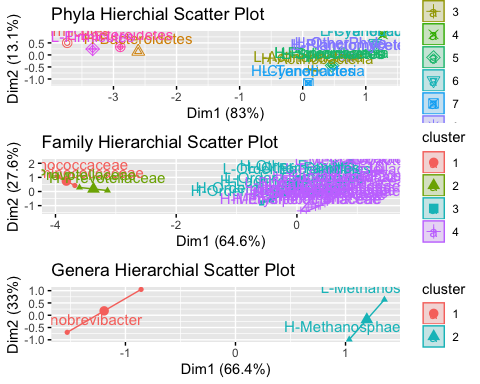
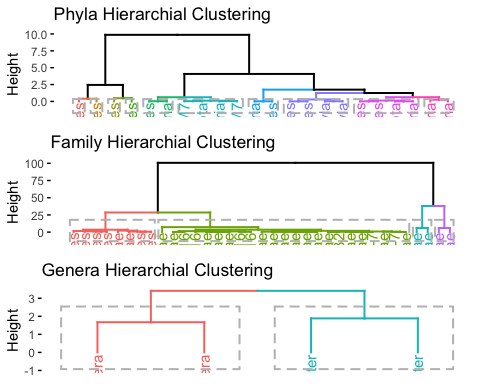
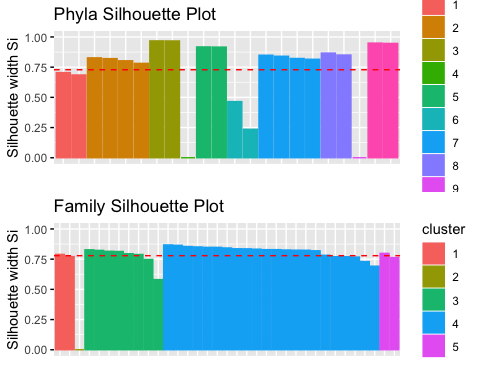
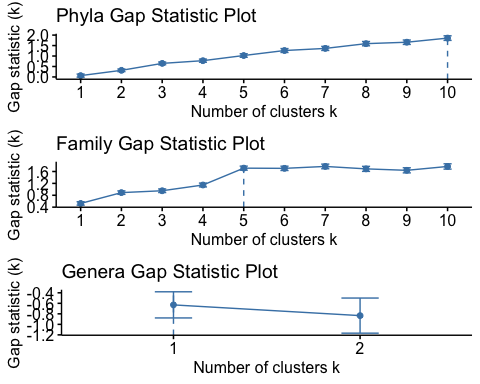
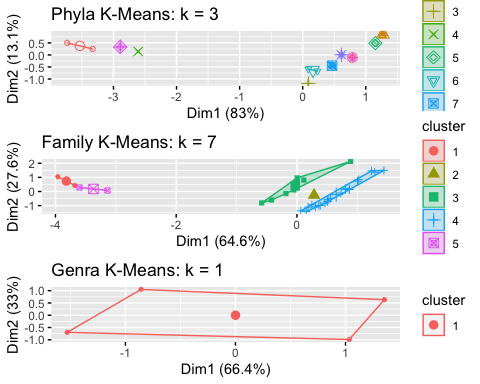


## cluster size ave.sil.width  
## 1 1 2 0.30  
## 2 2 2 0.38

# Combine and save figures

##   
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':  
##   
## combine



## Saving 5 x 4 in image

## Saving 5 x 4 in image  
## Saving 5 x 4 in image  
## Saving 5 x 4 in image  
## Saving 5 x 4 in image  
## Saving 5 x 4 in image

#Tidy data to run analysis  
  
#Combine data  
F1 <- rbind(familydata, familydata2)  
F1

|  |  |  |  |
| --- | --- | --- | --- |
| **Family** | **Beginning** | **End** | **P** |
| Ruminococcaceae | 26 | 40.3 | 0.17 |
| Prevotellaceae\* | 36.9 | 14.3 | 0.05 |
| Order Clostridiales | 5.93 | 8.4 | 0.08 |
| Order Bacteroidales | 5.94 | 7.49 | 0.15 |
| Lachnospiraceae | 5.19 | 7.7 | 0.29 |
| RF16 | 1.94 | 1.36 | 0.14 |
| Methanobacteriaceae\* | 1.24 | 2 | 0.01 |
| F16 | 1.05 | 2.11 | 0.09 |
| Paraprevotellaceae | 1.21 | 1.35 | 0.49 |
| S24-7 | 0.957 | 1.18 | 0.47 |
| Coriobacteriaceae | 0.86 | 1.06 | 0.29 |
| Erysipelotrichaceae\* | 1.16 | 0.734 | 0.01 |
| Bifidobacteriaceae | 1.45 | 0.312 | 0.11 |
| Spirochaetaceae | 1.14 | 0.475 | 0.14 |
| Streptococcaceae | 0.803 | 0.462 | 0.22 |
| Mogibacteriaceae | 0.477 | 0.774 | 0.14 |
| Succinivibrionaceae | 0.255 | 0.917 | 0.19 |
| Other Families | 7.51 | 9.03 | 0.59 |
| Ruminococcaceae\* | 20.1 | 39.3 | 0.04 |
| Prevotellaceae\* | 38 | 20.1 | 0.05 |
| Order Bacteroidales | 6.84 | 8.47 | 0.53 |
| Order Clostridiales | 5.51 | 7.12 | 0.37 |
| Lachnospiraceae | 5.9 | 5.86 | 0.98 |
| Bifidobacteriaceae | 6.23 | 0.317 | 0.32 |
| F16 | 1.81 | 2.05 | 0.85 |
| RF16 | 1.5 | 1.75 | 0.67 |
| Paraprevotellaceae | 1.33 | 1.5 | 0.64 |
| Methanobacteriaceae | 1.28 | 1.39 | 0.83 |
| Spirochaetaceae | 1.25 | 0.65 | 0.26 |
| Erysipelotrichaceae | 1.2 | 0.529 | 0.4 |
| Coriobacteriaceae | 0.707 | 0.758 | 0.88 |
| Succinivibrionaceae | 0.588 | 0.82 | 0.48 |
| Order RF32 | 0.446 | 0.932 | 0.48 |
| S24-7 | 0.494 | 0.862 | 0.23 |
| Other Families | 6.73 | 7.62 | 0.564 |

#Create new column with change in bacterial abundance over time  
F1 <- F1 %>% mutate(Abundance.Difference = (End - Beginning))  
F1 <- F1 %>% select(Family, Abundance.Difference)  
F1

|  |  |
| --- | --- |
| **Family** | **Abundance.Difference** |
| Ruminococcaceae | 14.4 |
| Prevotellaceae\* | -22.6 |
| Order Clostridiales | 2.47 |
| Order Bacteroidales | 1.55 |
| Lachnospiraceae | 2.51 |
| RF16 | -0.58 |
| Methanobacteriaceae\* | 0.77 |
| F16 | 1.06 |
| Paraprevotellaceae | 0.134 |
| S24-7 | 0.22 |
| Coriobacteriaceae | 0.198 |
| Erysipelotrichaceae\* | -0.425 |
| Bifidobacteriaceae | -1.14 |
| Spirochaetaceae | -0.66 |
| Streptococcaceae | -0.341 |
| Mogibacteriaceae | 0.297 |
| Succinivibrionaceae | 0.661 |
| Other Families | 1.52 |
| Ruminococcaceae\* | 19.1 |
| Prevotellaceae\* | -17.9 |
| Order Bacteroidales | 1.64 |
| Order Clostridiales | 1.61 |
| Lachnospiraceae | -0.0405 |
| Bifidobacteriaceae | -5.91 |
| F16 | 0.241 |
| RF16 | 0.252 |
| Paraprevotellaceae | 0.165 |
| Methanobacteriaceae | 0.112 |
| Spirochaetaceae | -0.605 |
| Erysipelotrichaceae | -0.671 |
| Coriobacteriaceae | 0.0509 |
| Succinivibrionaceae | 0.232 |
| Order RF32 | 0.486 |
| S24-7 | 0.368 |
| Other Families | 0.891 |

str(F1)

## Classes 'tbl\_df', 'tbl' and 'data.frame': 35 obs. of 2 variables:  
## $ Family : chr "Ruminococcaceae" "Prevotellaceae\*" "Order Clostridiales" "Order Bacteroidales" ...  
## $ Abundance.Difference: num 14.36 -22.6 2.47 1.55 2.51 ...

#Duplicate/create new family column in order to create Bacteria Family as a factor  
F1 <- F1 %>% mutate(Bacterial.Family = Family)  
str(F1)

## Classes 'tbl\_df', 'tbl' and 'data.frame': 35 obs. of 3 variables:  
## $ Family : chr "Ruminococcaceae" "Prevotellaceae\*" "Order Clostridiales" "Order Bacteroidales" ...  
## $ Abundance.Difference: num 14.36 -22.6 2.47 1.55 2.51 ...  
## $ Bacterial.Family : chr "Ruminococcaceae" "Prevotellaceae\*" "Order Clostridiales" "Order Bacteroidales" ...

F1$Family=as.factor(F1$Family)  
F1$Family=as.numeric(F1$Family)  
lapply(F1, levels)

## $Family  
## NULL  
##   
## $Abundance.Difference  
## NULL  
##   
## $Bacterial.Family  
## NULL

F1$Bacterial.Family=as.factor(F1$Bacterial.Family)  
lapply(F1, levels)

## $Family  
## NULL  
##   
## $Abundance.Difference  
## NULL  
##   
## $Bacterial.Family  
## [1] "Bifidobacteriaceae" "Coriobacteriaceae" "Erysipelotrichaceae"   
## [4] "Erysipelotrichaceae\*" "F16" "Lachnospiraceae"   
## [7] "Methanobacteriaceae" "Methanobacteriaceae\*" "Mogibacteriaceae"   
## [10] "Order Bacteroidales" "Order Clostridiales" "Order RF32"   
## [13] "Other Families" "Paraprevotellaceae" "Prevotellaceae\*"   
## [16] "RF16" "Ruminococcaceae" "Ruminococcaceae\*"   
## [19] "S24-7" "Spirochaetaceae" "Streptococcaceae"   
## [22] "Succinivibrionaceae"

F1$Family=as.numeric(F1$Family)  
lapply(F1, levels)

## $Family  
## NULL  
##   
## $Abundance.Difference  
## NULL  
##   
## $Bacterial.Family  
## [1] "Bifidobacteriaceae" "Coriobacteriaceae" "Erysipelotrichaceae"   
## [4] "Erysipelotrichaceae\*" "F16" "Lachnospiraceae"   
## [7] "Methanobacteriaceae" "Methanobacteriaceae\*" "Mogibacteriaceae"   
## [10] "Order Bacteroidales" "Order Clostridiales" "Order RF32"   
## [13] "Other Families" "Paraprevotellaceae" "Prevotellaceae\*"   
## [16] "RF16" "Ruminococcaceae" "Ruminococcaceae\*"   
## [19] "S24-7" "Spirochaetaceae" "Streptococcaceae"   
## [22] "Succinivibrionaceae"

F1$Family=as.factor(F1$Family)  
lapply(F1, levels)

## $Family  
## [1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12" "13" "14"  
## [15] "15" "16" "17" "18" "19" "20" "21" "22"  
##   
## $Abundance.Difference  
## NULL  
##   
## $Bacterial.Family  
## [1] "Bifidobacteriaceae" "Coriobacteriaceae" "Erysipelotrichaceae"   
## [4] "Erysipelotrichaceae\*" "F16" "Lachnospiraceae"   
## [7] "Methanobacteriaceae" "Methanobacteriaceae\*" "Mogibacteriaceae"   
## [10] "Order Bacteroidales" "Order Clostridiales" "Order RF32"   
## [13] "Other Families" "Paraprevotellaceae" "Prevotellaceae\*"   
## [16] "RF16" "Ruminococcaceae" "Ruminococcaceae\*"   
## [19] "S24-7" "Spirochaetaceae" "Streptococcaceae"   
## [22] "Succinivibrionaceae"

saveRDS(F1, file = here("././results/F1.rds"))  
  
#Create new data frame to add in RFI status  
RFI\_Status <- c(2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,2,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1)  
CatRFI <- cut(RFI\_Status, breaks = c(0,1,2), labels =c("LowRFI", "HighRFI"))  
  
RFI\_Group <- data\_frame(CatRFI)

## Warning: `data\_frame()` is deprecated, use `tibble()`.  
## This warning is displayed once per session.

#Merge two dataframes   
F2 <-cbind(F1, CatRFI)  
F2

|  |  |  |  |
| --- | --- | --- | --- |
| **Family** | **Abundance.Difference** | **Bacterial.Family** | **CatRFI** |
| 17 | 14.4 | Ruminococcaceae | HighRFI |
| 15 | -22.6 | Prevotellaceae\* | HighRFI |
| 11 | 2.47 | Order Clostridiales | HighRFI |
| 10 | 1.55 | Order Bacteroidales | HighRFI |
| 6 | 2.51 | Lachnospiraceae | HighRFI |
| 16 | -0.58 | RF16 | HighRFI |
| 8 | 0.77 | Methanobacteriaceae\* | HighRFI |
| 5 | 1.06 | F16 | HighRFI |
| 14 | 0.134 | Paraprevotellaceae | HighRFI |
| 19 | 0.22 | S24-7 | HighRFI |
| 2 | 0.198 | Coriobacteriaceae | HighRFI |
| 4 | -0.425 | Erysipelotrichaceae\* | HighRFI |
| 1 | -1.14 | Bifidobacteriaceae | HighRFI |
| 20 | -0.66 | Spirochaetaceae | HighRFI |
| 21 | -0.341 | Streptococcaceae | HighRFI |
| 9 | 0.297 | Mogibacteriaceae | HighRFI |
| 22 | 0.661 | Succinivibrionaceae | HighRFI |
| 13 | 1.52 | Other Families | HighRFI |
| 18 | 19.1 | Ruminococcaceae\* | LowRFI |
| 15 | -17.9 | Prevotellaceae\* | LowRFI |
| 10 | 1.64 | Order Bacteroidales | LowRFI |
| 11 | 1.61 | Order Clostridiales | LowRFI |
| 6 | -0.0405 | Lachnospiraceae | LowRFI |
| 1 | -5.91 | Bifidobacteriaceae | LowRFI |
| 5 | 0.241 | F16 | LowRFI |
| 16 | 0.252 | RF16 | LowRFI |
| 14 | 0.165 | Paraprevotellaceae | LowRFI |
| 7 | 0.112 | Methanobacteriaceae | LowRFI |
| 20 | -0.605 | Spirochaetaceae | LowRFI |
| 3 | -0.671 | Erysipelotrichaceae | LowRFI |
| 2 | 0.0509 | Coriobacteriaceae | LowRFI |
| 22 | 0.232 | Succinivibrionaceae | LowRFI |
| 12 | 0.486 | Order RF32 | LowRFI |
| 19 | 0.368 | S24-7 | LowRFI |
| 13 | 0.891 | Other Families | LowRFI |

#Change name of RFI colunm  
names(F2)[1:4]<-c("Family", "Abundance\_Difference", "Bacterial.Family", "RFI\_Status")  
F2

|  |  |  |  |
| --- | --- | --- | --- |
| **Family** | **Abundance\_Difference** | **Bacterial.Family** | **RFI\_Status** |
| 17 | 14.4 | Ruminococcaceae | HighRFI |
| 15 | -22.6 | Prevotellaceae\* | HighRFI |
| 11 | 2.47 | Order Clostridiales | HighRFI |
| 10 | 1.55 | Order Bacteroidales | HighRFI |
| 6 | 2.51 | Lachnospiraceae | HighRFI |
| 16 | -0.58 | RF16 | HighRFI |
| 8 | 0.77 | Methanobacteriaceae\* | HighRFI |
| 5 | 1.06 | F16 | HighRFI |
| 14 | 0.134 | Paraprevotellaceae | HighRFI |
| 19 | 0.22 | S24-7 | HighRFI |
| 2 | 0.198 | Coriobacteriaceae | HighRFI |
| 4 | -0.425 | Erysipelotrichaceae\* | HighRFI |
| 1 | -1.14 | Bifidobacteriaceae | HighRFI |
| 20 | -0.66 | Spirochaetaceae | HighRFI |
| 21 | -0.341 | Streptococcaceae | HighRFI |
| 9 | 0.297 | Mogibacteriaceae | HighRFI |
| 22 | 0.661 | Succinivibrionaceae | HighRFI |
| 13 | 1.52 | Other Families | HighRFI |
| 18 | 19.1 | Ruminococcaceae\* | LowRFI |
| 15 | -17.9 | Prevotellaceae\* | LowRFI |
| 10 | 1.64 | Order Bacteroidales | LowRFI |
| 11 | 1.61 | Order Clostridiales | LowRFI |
| 6 | -0.0405 | Lachnospiraceae | LowRFI |
| 1 | -5.91 | Bifidobacteriaceae | LowRFI |
| 5 | 0.241 | F16 | LowRFI |
| 16 | 0.252 | RF16 | LowRFI |
| 14 | 0.165 | Paraprevotellaceae | LowRFI |
| 7 | 0.112 | Methanobacteriaceae | LowRFI |
| 20 | -0.605 | Spirochaetaceae | LowRFI |
| 3 | -0.671 | Erysipelotrichaceae | LowRFI |
| 2 | 0.0509 | Coriobacteriaceae | LowRFI |
| 22 | 0.232 | Succinivibrionaceae | LowRFI |
| 12 | 0.486 | Order RF32 | LowRFI |
| 19 | 0.368 | S24-7 | LowRFI |
| 13 | 0.891 | Other Families | LowRFI |

saveRDS(F2, file = here("././results/F2.rds"))

Linear Regression Model: Abundance ~RFI Status

#Simple  
#By default, the category that R chooses to be the reference/ baseline, is the first category that appears (ie. LowRFI). In LR model, the intercept refers to the estimated mean Y value for the reference group and the model coefficients, refer to expected changes in the mean Y-value relative to the reference group.   
  
#reference LowRFI  
mod1= lm(Abundance\_Difference ~ RFI\_Status, data = F2)  
tidy(mod1)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | -1.76e-10 | 1.62 | -1.09e-10 | 1 |
| RFI\_StatusHighRFI | 8.99e-10 | 2.26 | 3.98e-10 | 1 |

mod1sum <- summary(mod1)  
saveRDS(mod1sum, file = here("././results/mod1sum.rds"))  
  
#Multi  
mod2=lm(Abundance\_Difference ~ RFI\_Status + Bacterial.Family, data = F2 )  
mod2

##   
## Call:  
## lm(formula = Abundance\_Difference ~ RFI\_Status + Bacterial.Family,   
## data = F2)  
##   
## Coefficients:  
## (Intercept)   
## -3.6955   
## RFI\_StatusHighRFI   
## 0.3374   
## Bacterial.FamilyCoriobacteriaceae   
## 3.6511   
## Bacterial.FamilyErysipelotrichaceae   
## 3.0246   
## Bacterial.FamilyErysipelotrichaceae\*   
## 2.9329   
## Bacterial.FamilyF16   
## 4.1782   
## Bacterial.FamilyLachnospiraceae   
## 4.7623   
## Bacterial.FamilyMethanobacteriaceae   
## 3.8072   
## Bacterial.FamilyMethanobacteriaceae\*   
## 4.1277   
## Bacterial.FamilyMogibacteriaceae   
## 3.6551   
## Bacterial.FamilyOrder Bacteroidales   
## 5.1173   
## Bacterial.FamilyOrder Clostridiales   
## 5.5664   
## Bacterial.FamilyOrder RF32   
## 4.1819   
## Bacterial.FamilyOther Families   
## 4.7327   
## Bacterial.FamilyParaprevotellaceae   
## 3.6762   
## Bacterial.FamilyPrevotellaceae\*   
## -16.7430   
## Bacterial.FamilyRF16   
## 3.3625   
## Bacterial.FamilyRuminococcaceae   
## 17.7207   
## Bacterial.FamilyRuminococcaceae\*   
## 22.8168   
## Bacterial.FamilyS24-7   
## 3.8208   
## Bacterial.FamilySpirochaetaceae   
## 2.8940   
## Bacterial.FamilyStreptococcaceae   
## 3.0168   
## Bacterial.FamilySuccinivibrionaceae   
## 3.9737

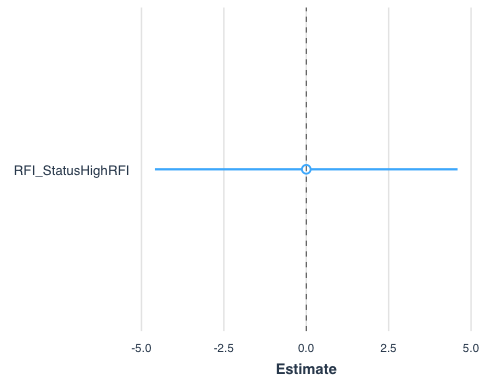
tidy(mod2)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | -3.7 | 1.08 | -3.41 | 0.00518 |
| RFI\_StatusHighRFI | 0.337 | 0.579 | 0.582 | 0.571 |
| Bacterial.FamilyCoriobacteriaceae | 3.65 | 1.48 | 2.47 | 0.0294 |
| Bacterial.FamilyErysipelotrichaceae | 3.02 | 1.83 | 1.65 | 0.125 |
| Bacterial.FamilyErysipelotrichaceae\* | 2.93 | 1.83 | 1.6 | 0.135 |
| Bacterial.FamilyF16 | 4.18 | 1.48 | 2.83 | 0.0152 |
| Bacterial.FamilyLachnospiraceae | 4.76 | 1.48 | 3.22 | 0.0073 |
| Bacterial.FamilyMethanobacteriaceae | 3.81 | 1.83 | 2.08 | 0.0598 |
| Bacterial.FamilyMethanobacteriaceae\* | 4.13 | 1.83 | 2.25 | 0.0438 |
| Bacterial.FamilyMogibacteriaceae | 3.66 | 1.83 | 2 | 0.0692 |
| Bacterial.FamilyOrder Bacteroidales | 5.12 | 1.48 | 3.46 | 0.00468 |
| Bacterial.FamilyOrder Clostridiales | 5.57 | 1.48 | 3.77 | 0.00268 |
| Bacterial.FamilyOrder RF32 | 4.18 | 1.83 | 2.28 | 0.0415 |
| Bacterial.FamilyOther Families | 4.73 | 1.48 | 3.2 | 0.00757 |
| Bacterial.FamilyParaprevotellaceae | 3.68 | 1.48 | 2.49 | 0.0285 |
| Bacterial.FamilyPrevotellaceae\* | -16.7 | 1.48 | -11.3 | 9.1e-08 |
| Bacterial.FamilyRF16 | 3.36 | 1.48 | 2.28 | 0.0419 |
| Bacterial.FamilyRuminococcaceae | 17.7 | 1.83 | 9.67 | 5.13e-07 |
| Bacterial.FamilyRuminococcaceae\* | 22.8 | 1.83 | 12.5 | 3.19e-08 |
| Bacterial.FamilyS24-7 | 3.82 | 1.48 | 2.59 | 0.0238 |
| Bacterial.FamilySpirochaetaceae | 2.89 | 1.48 | 1.96 | 0.0737 |
| Bacterial.FamilyStreptococcaceae | 3.02 | 1.83 | 1.65 | 0.126 |
| Bacterial.FamilySuccinivibrionaceae | 3.97 | 1.48 | 2.69 | 0.0197 |

#To check for significant varibles   
mod2sum <- summary(mod2)  
saveRDS(mod2sum, file = here("././results/mod2sum.rds"))  
  
#Approximately 98% of variation in family abundance over time can be explained by RFI status and classification of bacterial families.   
#There are a lot of signif values and the p-value overall is small. This linear model appears to be a good fit for this data set.

Plotting Linear Regression Model

#Single model  
  
plot\_summs(mod1)



#Differing scales of the varibles   
plotmod2 <- plot\_summs(mod2, scale = TRUE)  
saveRDS(plotmod2, file = here("././results/plotmod2.rds"))  
  
#The default width of the confidencfe interval is .95  
plotmod2sum <- plot\_summs(mod2, scale = TRUE, inner\_ci\_level = .9)  
saveRDS(plotmod2sum, file = here("././results/plotmod2sum.rds"))  
  
#Plot coefficient uncertainty as normal distributions  
plotmod2sum2 <- plot\_summs(mod2, scale = TRUE, plot.distributions = TRUE, inner\_ci\_level = .9)  
  
saveRDS(plotmod2sum2, file = here("././results/plotmod2sum2.rds"))

Table Outputts for Word/RMD

expmod2 <- export\_summs(mod2, scale = TRUE)  
  
  
#add confidence intervals   
expmod2.2 <- export\_summs(mod2, scale = TRUE, error\_format = "[{conf.low}, {conf.high}]")  
  
  
#add p values  
expmod2.3 <- export\_summs(mod2, scale = TRUE, error\_format = "[{statistic}, p = {p.value}]")  
saveRDS(expmod2.3, file = here("././results/expmod2.3.rds"))

Looking at other models: Logistic Regression Model

#Change RFI\_Status baack to numbers   
levels(F2$RFI\_Status) <- c("1", "2")  
lapply(F2, levels)

## $Family  
## [1] "1" "2" "3" "4" "5" "6" "7" "8" "9" "10" "11" "12" "13" "14"  
## [15] "15" "16" "17" "18" "19" "20" "21" "22"  
##   
## $Abundance\_Difference  
## NULL  
##   
## $Bacterial.Family  
## [1] "Bifidobacteriaceae" "Coriobacteriaceae" "Erysipelotrichaceae"   
## [4] "Erysipelotrichaceae\*" "F16" "Lachnospiraceae"   
## [7] "Methanobacteriaceae" "Methanobacteriaceae\*" "Mogibacteriaceae"   
## [10] "Order Bacteroidales" "Order Clostridiales" "Order RF32"   
## [13] "Other Families" "Paraprevotellaceae" "Prevotellaceae\*"   
## [16] "RF16" "Ruminococcaceae" "Ruminococcaceae\*"   
## [19] "S24-7" "Spirochaetaceae" "Streptococcaceae"   
## [22] "Succinivibrionaceae"   
##   
## $RFI\_Status  
## [1] "1" "2"

F2

|  |  |  |  |
| --- | --- | --- | --- |
| **Family** | **Abundance\_Difference** | **Bacterial.Family** | **RFI\_Status** |
| 17 | 14.4 | Ruminococcaceae | 2 |
| 15 | -22.6 | Prevotellaceae\* | 2 |
| 11 | 2.47 | Order Clostridiales | 2 |
| 10 | 1.55 | Order Bacteroidales | 2 |
| 6 | 2.51 | Lachnospiraceae | 2 |
| 16 | -0.58 | RF16 | 2 |
| 8 | 0.77 | Methanobacteriaceae\* | 2 |
| 5 | 1.06 | F16 | 2 |
| 14 | 0.134 | Paraprevotellaceae | 2 |
| 19 | 0.22 | S24-7 | 2 |
| 2 | 0.198 | Coriobacteriaceae | 2 |
| 4 | -0.425 | Erysipelotrichaceae\* | 2 |
| 1 | -1.14 | Bifidobacteriaceae | 2 |
| 20 | -0.66 | Spirochaetaceae | 2 |
| 21 | -0.341 | Streptococcaceae | 2 |
| 9 | 0.297 | Mogibacteriaceae | 2 |
| 22 | 0.661 | Succinivibrionaceae | 2 |
| 13 | 1.52 | Other Families | 2 |
| 18 | 19.1 | Ruminococcaceae\* | 1 |
| 15 | -17.9 | Prevotellaceae\* | 1 |
| 10 | 1.64 | Order Bacteroidales | 1 |
| 11 | 1.61 | Order Clostridiales | 1 |
| 6 | -0.0405 | Lachnospiraceae | 1 |
| 1 | -5.91 | Bifidobacteriaceae | 1 |
| 5 | 0.241 | F16 | 1 |
| 16 | 0.252 | RF16 | 1 |
| 14 | 0.165 | Paraprevotellaceae | 1 |
| 7 | 0.112 | Methanobacteriaceae | 1 |
| 20 | -0.605 | Spirochaetaceae | 1 |
| 3 | -0.671 | Erysipelotrichaceae | 1 |
| 2 | 0.0509 | Coriobacteriaceae | 1 |
| 22 | 0.232 | Succinivibrionaceae | 1 |
| 12 | 0.486 | Order RF32 | 1 |
| 19 | 0.368 | S24-7 | 1 |
| 13 | 0.891 | Other Families | 1 |

#RFI\_Status ~ Abundance\_Difference  
mod3 <- glm(RFI\_Status ~ Abundance\_Difference, family = "binomial", data = F2)  
tidy(mod3)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | 0.0572 | 0.338 | 0.169 | 0.866 |
| Abundance\_Difference | 2.14e-11 | 0.0522 | 4.1e-10 | 1 |

mod3sum <- summary(mod3)  
saveRDS(mod3sum, file = here("././results/mod3sum.rds"))  
  
  
  
#RFI\_Status ~ Family  
mod4 <- glm(RFI\_Status ~ Family, family = "binomial", data = F2)  
tidy(mod4)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | 3.39e-15 | 1.41 | 2.39e-15 | 1 |
| Family2 | -3.31e-15 | 2 | -1.66e-15 | 1 |
| Family3 | -18.6 | 6.52e+03 | -0.00285 | 0.998 |
| Family4 | 18.6 | 6.52e+03 | 0.00285 | 0.998 |
| Family5 | -3.35e-15 | 2 | -1.67e-15 | 1 |
| Family6 | -4.23e-15 | 2 | -2.11e-15 | 1 |
| Family7 | -18.6 | 6.52e+03 | -0.00285 | 0.998 |
| Family8 | 18.6 | 6.52e+03 | 0.00285 | 0.998 |
| Family9 | 18.6 | 6.52e+03 | 0.00285 | 0.998 |
| Family10 | -2.4e-15 | 2 | -1.2e-15 | 1 |
| Family11 | -2.77e-15 | 2 | -1.38e-15 | 1 |
| Family12 | -18.6 | 6.52e+03 | -0.00285 | 0.998 |
| Family13 | -3.76e-15 | 2 | -1.88e-15 | 1 |
| Family14 | -4.12e-15 | 2 | -2.06e-15 | 1 |
| Family15 | -3.64e-15 | 2 | -1.82e-15 | 1 |
| Family16 | -4.32e-15 | 2 | -2.16e-15 | 1 |
| Family17 | 18.6 | 6.52e+03 | 0.00285 | 0.998 |
| Family18 | -18.6 | 6.52e+03 | -0.00285 | 0.998 |
| Family19 | -4.15e-15 | 2 | -2.08e-15 | 1 |
| Family20 | -4.08e-15 | 2 | -2.04e-15 | 1 |
| Family21 | 18.6 | 6.52e+03 | 0.00285 | 0.998 |
| Family22 | -3.77e-15 | 2 | -1.89e-15 | 1 |

summary(mod4)

##   
## Call:  
## glm(formula = RFI\_Status ~ Family, family = "binomial", data = F2)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.17741 -1.17741 0.00013 1.17741 1.17741   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 3.386e-15 1.414e+00 0.000 1.000  
## Family2 -3.312e-15 2.000e+00 0.000 1.000  
## Family3 -1.857e+01 6.523e+03 -0.003 0.998  
## Family4 1.857e+01 6.523e+03 0.003 0.998  
## Family5 -3.346e-15 2.000e+00 0.000 1.000  
## Family6 -4.229e-15 2.000e+00 0.000 1.000  
## Family7 -1.857e+01 6.523e+03 -0.003 0.998  
## Family8 1.857e+01 6.523e+03 0.003 0.998  
## Family9 1.857e+01 6.523e+03 0.003 0.998  
## Family10 -2.401e-15 2.000e+00 0.000 1.000  
## Family11 -2.767e-15 2.000e+00 0.000 1.000  
## Family12 -1.857e+01 6.523e+03 -0.003 0.998  
## Family13 -3.757e-15 2.000e+00 0.000 1.000  
## Family14 -4.124e-15 2.000e+00 0.000 1.000  
## Family15 -3.643e-15 2.000e+00 0.000 1.000  
## Family16 -4.324e-15 2.000e+00 0.000 1.000  
## Family17 1.857e+01 6.523e+03 0.003 0.998  
## Family18 -1.857e+01 6.523e+03 -0.003 0.998  
## Family19 -4.152e-15 2.000e+00 0.000 1.000  
## Family20 -4.078e-15 2.000e+00 0.000 1.000  
## Family21 1.857e+01 6.523e+03 0.003 0.998  
## Family22 -3.775e-15 2.000e+00 0.000 1.000  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 48.492 on 34 degrees of freedom  
## Residual deviance: 36.044 on 13 degrees of freedom  
## AIC: 80.044  
##   
## Number of Fisher Scoring iterations: 17

mod4sum <- summary(mod4)  
saveRDS(mod4sum, file = here("././results/mod4sum.rds"))  
  
  
#RFI\_Status ~ Family + Abundance\_Difference +Bacterial. Family  
mod5 <- glm(RFI\_Status ~ Family + Abundance\_Difference + Bacterial.Family, family = "binomial", data = F2)  
tidy(mod5)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **term** | **estimate** | **std.error** | **statistic** | **p.value** |
| (Intercept) | 1.2 | 2.11 | 0.569 | 0.57 |
| Family2 | -1.24 | 2.57 | -0.484 | 0.629 |
| Family3 | -19.5 | 6.52e+03 | -0.003 | 0.998 |
| Family4 | 17.5 | 6.52e+03 | 0.00268 | 0.998 |
| Family5 | -1.42 | 2.71 | -0.526 | 0.599 |
| Family6 | -1.62 | 2.88 | -0.563 | 0.573 |
| Family7 | -19.8 | 6.52e+03 | -0.00304 | 0.998 |
| Family8 | 17.1 | 6.52e+03 | 0.00262 | 0.998 |
| Family9 | 17.3 | 6.52e+03 | 0.00265 | 0.998 |
| Family10 | -1.74 | 2.97 | -0.588 | 0.557 |
| Family11 | -1.9 | 3.1 | -0.611 | 0.541 |
| Family12 | -19.9 | 6.52e+03 | -0.00306 | 0.998 |
| Family13 | -1.61 | 2.86 | -0.564 | 0.572 |
| Family14 | -1.25 | 2.58 | -0.486 | 0.627 |
| Family15 | 5.71 | 7.24 | 0.788 | 0.43 |
| Family16 | -1.15 | 2.51 | -0.457 | 0.648 |
| Family17 | 12.5 | 6.52e+03 | 0.00191 | 0.998 |
| Family18 | -26.3 | 6.52e+03 | -0.00403 | 0.997 |
| Family19 | -1.3 | 2.61 | -0.498 | 0.618 |
| Family20 | -0.986 | 2.4 | -0.41 | 0.681 |
| Family21 | 17.5 | 6.52e+03 | 0.00268 | 0.998 |
| Family22 | -1.35 | 2.65 | -0.51 | 0.61 |
| Abundance\_Difference | 0.341 | 0.412 | 0.826 | 0.409 |

summary(mod4)

##   
## Call:  
## glm(formula = RFI\_Status ~ Family, family = "binomial", data = F2)  
##   
## Deviance Residuals:   
## Min 1Q Median 3Q Max   
## -1.17741 -1.17741 0.00013 1.17741 1.17741   
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) 3.386e-15 1.414e+00 0.000 1.000  
## Family2 -3.312e-15 2.000e+00 0.000 1.000  
## Family3 -1.857e+01 6.523e+03 -0.003 0.998  
## Family4 1.857e+01 6.523e+03 0.003 0.998  
## Family5 -3.346e-15 2.000e+00 0.000 1.000  
## Family6 -4.229e-15 2.000e+00 0.000 1.000  
## Family7 -1.857e+01 6.523e+03 -0.003 0.998  
## Family8 1.857e+01 6.523e+03 0.003 0.998  
## Family9 1.857e+01 6.523e+03 0.003 0.998  
## Family10 -2.401e-15 2.000e+00 0.000 1.000  
## Family11 -2.767e-15 2.000e+00 0.000 1.000  
## Family12 -1.857e+01 6.523e+03 -0.003 0.998  
## Family13 -3.757e-15 2.000e+00 0.000 1.000  
## Family14 -4.124e-15 2.000e+00 0.000 1.000  
## Family15 -3.643e-15 2.000e+00 0.000 1.000  
## Family16 -4.324e-15 2.000e+00 0.000 1.000  
## Family17 1.857e+01 6.523e+03 0.003 0.998  
## Family18 -1.857e+01 6.523e+03 -0.003 0.998  
## Family19 -4.152e-15 2.000e+00 0.000 1.000  
## Family20 -4.078e-15 2.000e+00 0.000 1.000  
## Family21 1.857e+01 6.523e+03 0.003 0.998  
## Family22 -3.775e-15 2.000e+00 0.000 1.000  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 48.492 on 34 degrees of freedom  
## Residual deviance: 36.044 on 13 degrees of freedom  
## AIC: 80.044  
##   
## Number of Fisher Scoring iterations: 17